

b.) Amendments to Specification

Please amend the paragraph at page 6, lines 16-38 to read as follows.

In another embodiment, an EBI-3-alt family member is identified based on the presence of an “N-terminal EBI-3-like domain” in the protein or corresponding nucleic acid molecule. As used herein, the term “N-terminal EBI-3-like domain” includes a protein domain which is about 30-80, preferably about 40-70, most preferably about 50-60 amino acid residues in length and has a primary structure that is 90%, 91%, 92%, 93%, 94%, 95,%, 96%, 97%, 98%, 99%, or more identical to a portion of the EBI-3 protein. In a preferred embodiment, the portion of the EBI-3 protein to which the N-terminal EBI-3-like domain corresponds is the N-terminal portion of the human EBI-3 protein (*e.g.*, from about amino acid position 1 to about amino acid position 54 of human EBI-3; SEQ ID NO:4). In another embodiment, an “N-terminal EBI-3-like domain” contains at least one “receptor_cytokines_1” signature sequence. As used herein, a “receptor_cytokines_1” signature sequence is a sequence routinely found towards the N-terminal portion of the extracellular domain of a number of receptors for lymphokines, hematopoietic growth factors, and hormone related molecules. The cytokine receptor signature sequence has the consensus pattern C-[LVFYR]-x(7,8)-[STIVDN]-C-x-W (SEQ ID NO:5), wherein the two conserved cysteine residues can be linked by a disulfide bond. The signature sequence has been assigned the name “receptor_cytokines_1” and the ProSite accession number PS00241 (<http://www.expasy.ch/prosite>). A “receptor_cytokines_1” signature sequence can be found in the N-terminal EBI-3-like domain of the human EBI-3-alt protein from about amino acids 35-48 (SEQ ID NO:2). In addition, the receptor_cytokines_1 signature

sequence of the human EBI-3-alt protein contains the pair of conserved cysteine residues described above (cys 35 and cys 46 of SEQ ID NO:2).